

# Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

Inventor(s): Attie/Stoehr/Schueler/Clee

Application No.:

Docket Number: 960296.99080

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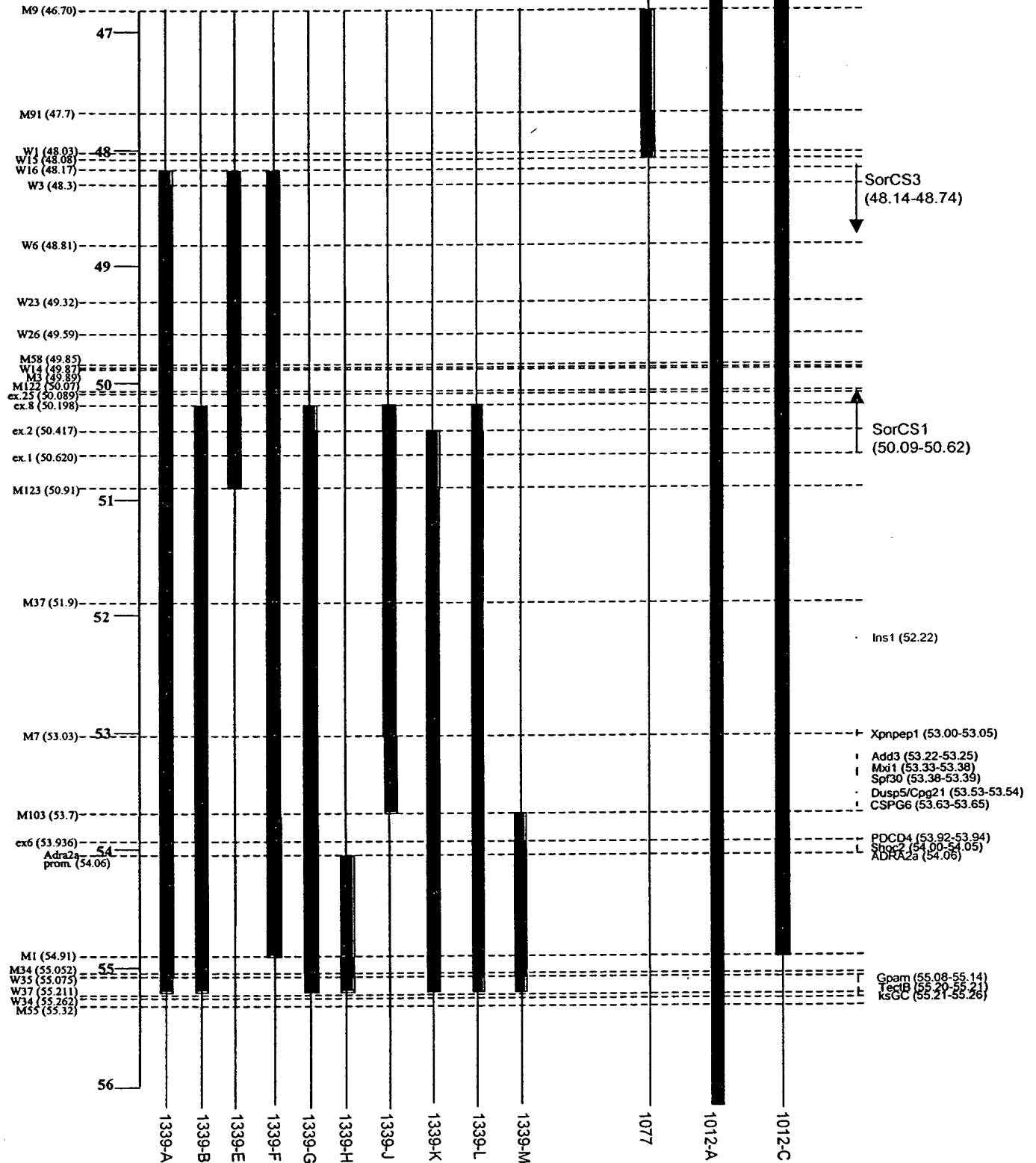


FIG 1

Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES  
Inventor(s): Attie/Stoehr/Schueler/Clee  
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Sequence 1: mSorLA 2033 aa  
Sequence 2: mSort 825 aa  
Sequence 3: Vps10p 1577 aa  
Sequence 4: mCS2 1159 aa  
Sequence 5: hCS3 1223 aa  
Sequence 6: mCS3 1219 aa  
Sequence 7: mCS1a 1147 aa  
Sequence 8: mCS1b 1167 aa  
Sequence 9: mCS1c 1178 aa  
Sequence 10: hCS1 1168 aa  
Aligning...

Sequences (1:2) Aligned. Score: 20  
Sequences (1:3) Aligned. Score: 8  
Sequences (1:4) Aligned. Score: 18  
Sequences (1:5) Aligned. Score: 16  
Sequences (1:6) Aligned. Score: 15  
Sequences (1:7) Aligned. Score: 13  
Sequences (1:8) Aligned. Score: 14  
Sequences (1:9) Aligned. Score: 13  
Sequences (1:10) Aligned. Score: 14  
Sequences (2:3) Aligned. Score: 16  
Sequences (2:4) Aligned. Score: 20  
Sequences (2:5) Aligned. Score: 20  
Sequences (2:6) Aligned. Score: 20  
Sequences (2:7) Aligned. Score: 21  
Sequences (2:8) Aligned. Score: 21  
Sequences (2:9) Aligned. Score: 20  
Sequences (2:10) Aligned. Score: 21  
Sequences (3:4) Aligned. Score: 11  
Sequences (3:5) Aligned. Score: 11  
Sequences (3:6) Aligned. Score: 11  
Sequences (3:7) Aligned. Score: 10  
Sequences (3:8) Aligned. Score: 11  
Sequences (3:9) Aligned. Score: 10

Sequences (3:10) Aligned. Score: 10  
Sequences (4:5) Aligned. Score: 42  
Sequences (4:6) Aligned. Score: 42  
Sequences (4:7) Aligned. Score: 42  
Sequences (4:8) Aligned. Score: 42  
Sequences (4:9) Aligned. Score: 43  
Sequences (4:10) Aligned. Score: 42  
Sequences (5:6) Aligned. Score: 92  
Sequences (5:7) Aligned. Score: 63  
Sequences (5:8) Aligned. Score: 62  
Sequences (5:9) Aligned. Score: 64  
Sequences (5:10) Aligned. Score: 63  
Sequences (6:7) Aligned. Score: 63  
Sequences (6:8) Aligned. Score: 62  
Sequences (6:9) Aligned. Score: 63  
Sequences (6:10) Aligned. Score: 61  
Sequences (7:8) Aligned. Score: 98  
Sequences (7:9) Aligned. Score: 97  
Sequences (7:10) Aligned. Score: 91  
Sequences (8:9) Aligned. Score: 96  
Sequences (8:10) Aligned. Score: 93  
Sequences (9:10) Aligned. Score: 90

CLUSTAL W (1.82) multiple sequence alignment

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mSorLA      YA QYLWITFDFCST IHGFSIPFRAAD LLLHSKASNLLL GFDRSHPNKQLW KSDDFGQTWI 60
mSort      -----
Vps10p      -----MILLH 5

      ..      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

mSorLA      MI QEHVKSFSWGID PYDQPNAIYIER HEPFGFSTVLRSTDFQSRNQEVILEEVRDFQL 120
mSort      -----
Vps10p      FV YSLWALLLIPLI NAEFTPKVTKT IAQDSFEILSFDDSNLIRKQDAS VTISFDDGET 65
      .. ..      . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .

mSorLA      RD KYMFATKVHLP GSQQQSSVQLWV SFGKPMRAAQFVTKHPINEYYIA DAAEDQVQVFC 180
mSort      -----MERPRG AADG----- 10
Vps10p      WE KVEGIEDEITWI YIDPFNRHRAVATSMYERLYITNDQGKSWERITLPDSEK---NI 122
mCS2      -----MA HRGPPSAPKRP GPTAPDRSFQA 24
hCS3      -N MEAARTERPAGR PGAPLVRTGLLLLSTWVLAGEIT WDATGGPGRPAPASRPALSP 59
mCS3      -- MEAAGTERPAGWPGAPLARTGLLLLSTWVLAGEIT WGATGGPGRLVS PASRPPVLPP 58
mCS1a      MG KVGAGDGYAG- LSALLAGAGLLML-----LAPGVCSSLSCCPPQHPSSTPR----RT 50
mCS1b      MG KVGAGDGSSAG- LSALLAGAGLLML-----LAPGVCSSLSCCPPQHPSSTPR----RT 50
mCS1c      MG KVGAGDGSSAG- LSALLAGAGLLML-----LAPGVCSSLSCCPPQHPSSTPR----RT 50
hCS1      MG KVGAGGGSQAR- LSALLAGAGLLIL-----CAPGVCSSGSCCPSHPSSAPR----SA 50
                                         T50->I

mSorLA      VSHSNNSTNLYISE AGLKFSLSLEN VLYSPGGAGSD TLVRYFANEPPA DFHRVEGLQG 240
mSort      -----LLRWPLGLLLLLQLLPPAAV G---QDRLDAPPPAPPLLRWAGP ----- 51
Vps10p      SS RGCYIETHPLNK NYFLAKCNYCEK TEVDNEENSGDEEGAPVIFNITRCTDKVFASNDG 182
mCS2      LLPPCWPRSWPLLLLLLVLAACGAM GRSPQGRQGGPG VQITRLLPAGRT ----- 74
hCS3      LS PRAVASQWPEELASARRAAVLGRR AGPELLPQQGGG RGGEMQVEAGGTSPAGERRGRG 119
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FIG 2A

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mCS3	LLPRAAENRWPEELASARRAAAPRRSRLEPL SQASR---	GEIR TEAGMSPEGAR WVPG 115
mCS1a	LT PRGFPHPGPLGR APATPPPLFMR-----	PLFAVAPG DRALFLERAGGS -----R 96
mCS1b	LT PRGFPHPGPLGR APATPPPLFMR-----	PLFAVAPG DRALFLERAGGS -----R 96
mCS1c	LT PRGFPHPGPLGR APATPPPLFMR-----	PLFAVAPG DRALFLERAGGS -----R 96
hCS1	ST PRGFSHQRPGR APATPLPLVVR-----	PLFSVAPG DRALSRLERARGT -----G 96
mSorLA	VY IATLINGSMNEE NMRSVITFDKGGTWEFLQAPFTGYGEKINCELSQGCSLHLAQRLS	300
mSort	-----VGVSWGLR AAPGGPVPRAG RWRRGAPAEDQD CGRLP-----	88
Vps10p	GK SFSEIKKSLE -R NENSAISISDCG FAKTGKDSDESSTDISIICLFQNM QLIMDEFSS-	240
mCS2	--ESGDRKDQPQR ESEPSVPLGLPGSASGPSTDGAPAPGKRRARAVPVAGAASASR--	129
hCS3	IPAPAKLGGAARRSRRAQPPITQERGD AWATAPADGSR--	GSRPLAKGSREEVKAPRAGG- 176
mCS3	IP SPSQAGSARRTRRAQPPSPLERGD SWATALADGAK--	GSRPHTKGSREEVRATRGTG- 172
mCS1a	VS VATAARSGRRRR SGTEPEKIEPGE GASRSRDMLKD GGQQQLGTGARD PGKATFRF--	154
mCS1b	VS VATAARSGRRRR SGTEPEKIEPGE GASRSRDMLKD GGQQQLGTGARD PGKATFRF--	154
mCS1c	VS VATAARSGRRRR SGTEPEKIEPGE GASRSRDMLKD GGQQQLGTGARD PGKATFRF--	154
hCS1	AS MAVAARSGRRRR SGADQEKAERGE GASRSPRGVLRD GGQQEPGTRE RD PDKATFRF--	154
	^furin? . ^furin? . :	:
mSorLA	QLNLNQLRRMPILS KESAPGLIATGSVGKNLASKTNV YISSSAGARWRE ALPGPHYTTW	360
mSort	-----DFIA KLNNTHQHVFDDLSGSVSLSW	114
Vps10p	-----PYTES KLVLTDDWGKSL KEFDQFKDKV	267
mCS2	-----AQV SLISTSFVLKGD ATHNQAMVHW	154
hCS3	-----SAAEDL RLPSTSFALTGD SAHNQAMVHW	204
mCS3	-----ASTEEL RLPSTSFALTGD SAHNQAMVHW	200
mCS1a	-----MEEL RLSTTTFALTGD SAHNQAMVHW	180
mCS1b	-----MEEL RLSTTTFALTGD SAHNQAMVHW	180
mCS1c	-----MEEL RLSTTTFALTGD SAHNQAMVHW	180
hCS1	-----MEEL RLSTTTFALTGD SAHNQAMVHW	180
	. . . : . . . : . :	: . :
mSorLA	GD HGGIIIMAIQAQM ETNELKYSTNEG ETWKTFVFSEKPVFVYGILLTEPGE KSTVFTIFGS	420
mSort	VG DSTGVILVLTTF QVPLVIVSFGQS KLYRSEDYGN---	FKDITNLINNTFI RTEFGM 170
Vps10p	VNGYRIKLSHMVVI TQGDYNDMSSM DVVWSNDLSNFK MAYMPTQLRHSM GGEIYEDAMG	327
mCS2	TG ENSSVILILTKEYH -ADMGVLESSLRSSDFGTT---	YTKLTLQPG VTTVIDNF-- 207
hCS3	SGHNSSVILILTKL YD-FNLGSVTESSLWRSTDYGT---	YEKLNDKVG LKTIVLSYL-- 257
mCS3	SGHNSSVILILTKL YD-FNLGSVTESSLWRSDYGT---	YEKLNDKVG LKTIVLSYL-- 253
mCS1a	SGHNSSVILILTKL YD-YNLGSITESSLWRSTDYGT---	YEKLNDKVG LKTIVLSYL-- 233
mCS1b	SGHNSSVILILTKL YD-YNLGSITESSLWRSTDYGT---	YEKLNDKVG LKTIVLSYL-- 233
mCS1c	SGHNSSVILILTKL YD-YNLGSITESSLWRSTDYGT---	YEKLNDKVG LKTIVLSYL-- 233
hCS1	SGHNSSVILILTKL YD-YNLGSITESSLWRSTDYGT---	YEKLNDKVG LKTIVLSYL-- 233
	.	:
mSorLA	NK ESVHSWLILQVN ATDALGVPCTEN DYKLWSPSDERGNECLLGHKTVFKRRTPHATCFN	480
mSort	-----AIGPENSGKVILTAEVSG -----	188
Vps10p	-----RIILPMS RERSDQEED-----	343
mCS2	-----YICPAN KRKIILVSSSL-----	224
hCS3	-----YVNPTN KRKIMLLSD-----	272
mCS3	-----YVNPTN KRKIMLLSD-----	268
mCS1a	-----YVCPTN KCKIMLLTD-----	248
mCS1b	-----YVCPTN KCKIMLLTD-----	248
mCS1c	-----YVCPTN KCKIMLLTD-----	248
hCS1	-----YVCPTN KCKIMLLTD-----	248
	. . . : . . . : . :	: . . : . . . : . :
mSorLA	GEDFDRPVVSNCSCTREDYECDFGF KMSEDLSLEVCPDPDEFFGPKYPSPVPVPCVPGSSY	540
mSort	GS RGRVFRSSDFA KNFVQTDLPHFP ----	LTOQMYS PQNSDYLLALST ENGLWVSKNF 243
Vps10p	KG IVSEILISDSQG LKFSPIPWANE VFG -YINLYQPTYLKGMTIASLYPLSRRNRKKG	402
mCS2	GD REOSLFLTSTDEGATFOKYPVTFL-----	VETLLFH PKEEKDVLAYTKDSKLYVSSDL 278

**FIG 2B**

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hCS3      PEMESSILISSDEGATYQKY RLTFY-----IQSLLFHPKQEDWVLAYS LDQKLYSSMDF 326
mCS3      PE MESSVLISSDEG ATYQKYRLTFY-----IQSLLFH PKQEDWVLAYS LDQKLYSSMDF 322
mCS1a     PE IESSLLISSDEG ATYQKYRLNFI-----LQSLLFH PKQEDWILAYS SQDQKLYSSAEF 302
mCS1b     PE IESSLLISSDEG ATYQKYRLNFI-----LQSLLFH PKQEDWILAYS SQDQKLYSSAEF 302
mCS1c     PE IESSLLISSDEG ATYQKYRLNFI-----LQSLLFH PKQEDWILAYS SQDQKLYSSAEF 302
hCS1      PE IESSLLISSDEG ATYQKYRLNFI-----IQSLLFH PKQEDWILAYS SQDQKLYSSAEF 302
. . . . .

mSorLA    RR TRGYRKISGDTCSGGDVEARLEGE LVPCPLAEENEFILYAMRKFIYRY DLASGATEQL 600
mSort     G--EKWEEIHK-----AVCLAK WGPNNIIFFTTH VNGSCKADLGAL ELWRTSDLGK 292
Vps10p    AK GVKNGKGVTKISV DNGLTWTVLKVV DPNADSFDCDI TDFENC SLQNMF YTREGSTPTA 462
mCS2      G--KKWTLQERV T KDHVFWAVSGVDDDPNLVHVEAQD LSGGYRYTCL I YNCSAQPHIA 336
hCS3      G--RRWQLMHERIT PNRFYWSVAGLD KEADLVHMEVRT TDGYAHYLTCRI QECAETTRSG 384
mCS3      G--RRWQLMHERIT PNRFYWSVAGLD KEADLVHMEVRT ADGYAHYLTCRI QECAETTRSG 380
mCS1a     G--RRWQLIQESVVPNRFYWSVMGSS KEPDLVHLEART VDGH SIYLT CRM QNCTEANRNK 360
mCS1b     G--RRWQLIQESVVPNRFYWSVMGSS KEPDLVHLEART VDGH SIYLT CRM QNCTEANRNK 360
mCS1c     G--RRWQLIQESVVPNRFYWSVMGSS KEPDLVHLEART VDGH SIYLT CRM QNCTEANRNK 360
hCS1      G--RRWQLIQEGVVPNRFYWSVMGSN KEPDLVHLEART VDGH SHYLT CRM QNCTEANRNQ 360
. . . . .

mSorLA    PL SGLRAAVALDFGYERNCLYWSDLALDTIQRLCLNGSTGQEV I INSGLE TVEALAFEPL 660
mSort     TF KTIG-----VKIYSFG LGGRFLFASE 315
Vps10p    GILMTTG-----IV GDGSVFDWGDQR TPI SRDGGLTWK LAFDFPCLYAVG DYGNVIVAIP 517
mCS2      PF SGP-----IDRGS LT VQDEYIFLKA 358
hCS3      PFARS-----IDISSLVVQDEYIFIQV 406
mCS3      PFARS-----IDISSLVVQDEYIFIQV 402
mCS1a     PFPGY-----IDPDSLIVQDDYVVFVQL 382
mCS1b     PFPGY-----IDPDSLIVQDDYVVFVQL 382
mCS1c     PFPGY-----IDPDSLIVQDDYVVFVQL 382
hCS1      PFPGY-----IDPDSLIVQDHYVVFVQL 382
. . . . .

mSorLA    SQ LLYWVDAGFKKI EVANPDGDFRLT IVNSSVLD RPRALVLPQEGVMFW TDWGD LKPGI 720
mSort     MA DK---DTTRRIH VSTDQGD TWSMA QLP SVGQE QFYS ILAANEDMVFMH VDE----- 365
Vps10p    YN ADEDDDPQSEFYYS LDQGKTWTEYQLETTIYPNEVM NTPD GSGAKFILNG-----F 571
mCS2      TS -----TNRTKYVSYRRSDFVLM KLPKYALPKDLQ IISTDEQQVFVAVQE----- 405
hCS3      TT -----SGRASYYVS YRREAF AQI KLPKYS LPKDMH IISTDENQVF AAVQE----- 453
mCS3      TI -----GGRASYYVS YRREAF AQI KLPKYS LPKDMH IISTDENQVF AAVQE----- 449
mCS1a     TS -----GGRPHYVSYRRSPFAQM KLPKYALPKDMH VISTDENQVF AAVQE----- 429
mCS1b     TS -----GGRPHYVSYRRSPFAQM KLPKYALPKDMH VISTDENQVF AAVQE----- 429
mCS1c     TS -----GGRPHYVSYRRSPFAQM KLPKYALPKDMH VISTDENQVF AAVQE----- 429
hCS1      TS -----GGRPHYVSYRRNAFAQM KLPKYALPKDMH VISTDENQVF AAVQE----- 429
. . . . .

mSorLA    YR SYMDGSAAYRLV SEDVKWPNGISV DS-----QWIYWT DAYLDC IERITFSGQQ 770
mSort     ---PGDTGFGTIFTSDDRGIVYSKSL DR-----HLYTTTG---ETDFTNVTSLR 409
Vps10p    TLAHMDGTTNFIY AIDFSTAFNDKTC EENDFEDWNLAEGKCVNGVKYKIRRRKQDAQCLV 631
mCS2      ---WNQVD TYNLYQSDLRGVRYSLVL EN-----VRSSRQAENNV IDILEVRGVK 452
hCS3      ---WNQND TYNLYI SDTRGIYFTLAM EN-----IKSSRGLMGNI IELYEVAGIK 500
mCS3      ---WNQND TYNLYI SDTRGIYFTLAM EN-----IKSSRGLMGNI IELYEVAGIK 496
mCS1a     ---WNQND TYNLYI SDTRGVYFTLAL EN-----VRSSRGPEGNV MIDLYEVAGIK 476
mCS1b     ---WNQND TYNLYI SDTRGVYFTLAL EN-----VRSSRGPEGNV MIDLYEVAGIK 476
mCS1c     ---WNQND TYNLYI SDTRGVYFTLAL EN-----VRSSRGPEGNV MIDLYEVAGIK 476
hCS1      ---WNQND TYNLYI SDTRGVYFTLAL EN-----VQSSRGPEGNIMIDLYEVAGIK 476

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FIG 2C

# Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

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:: : :

mSorLA	RSVILDSLPHPYAIAVFKNEIYWDDWSQLSIFRAS KHSRSQVEILASQLTGLMDMKVFY K 830	
mSort	GV YITSTLSEDNSI QSMITFDQGGRW EHLRKP-ENSKC DA-----	448
Vps10p	KK VFEDLQLFETAC DKCTEADYECAF EFVRDATGKCVP DYN-----	L 673
mCS2	GVFLAN-QKVDGKV TTVITYNKGRDW DYLRPPSTDMNG KP-----	491
hCS3	GIFLAN-KKVDDQV KTYITYNKGRDW RLLQAPDVDLRGSP-----	539
mCS3	GIFLAN-KKVDDQV KTYITYNKGRDW RLLQAPDVDLRGSP-----	535
mCS1a	GMFLAN-KKIDNQV KTFITYNKGRDW RLLQAPDADLRG DP-----	515
mCS1b	GMFLAN-KKIDNQV KTFITYNKGRDW RLLQAPDADLRG DP-----	515
mCS1c	GMFLAN-KKIDNQV KTFITYNKGRDW RLLQAPDADLRG DP-----	515
hCS1	GMFLAN-KKIDNQV KTFITYNKGRDW RLLQAPDADLRG DP-----	515

: . : : . . . . .

mSorLA	GK NAGSNACVPQPCSLCLPKANNSK SCRCPEGVASSVLPsgdlmcdcpqgyqrknntcv 890
mSort	-----TAKNKNECSLHIHASYSISQ KLNVPMAPLSEP NAVGIVIAHG----- 490
Vps10p	IVLSDVCDKTKKKT VPKPLQLVKGD KCKKPMTVKSVD ISCEGVPKKG----- 721
mCS2	-----TNCQPPDCYLHLHLRWADNP YVSGTVH--TKD TAPGLIMGAG----- 531
hCS3	-----VHCLLPFCSLHLHLQLENP YSSGRIS--SKE TAPGLVVATG----- 579
mCS3	-----VHCLLPFCSLHLHLQLENP YSSGRIS--SKD TAPGLVVATG----- 575
mCS1a	-----VHCLLPYCSLHLHLKVS ENP YTSGIIA--SRD TAPSIIVASG----- 555
mCS1b	-----VHCLLPYCSLHLHLKVS ENP YTSGIIA--SRD TAPSIIVASG----- 555
mCS1c	-----VHCLLPYCSLHLHLKVS ENP YTSGIIA--SRD TAPSIIVASG----- 555
hCS1	-----VHCLLPYCSLHLHLKVS ENP YTSGIIA--SKD TAPSIIVASG----- 555

: . : : . . . . .

mSorLA	KEENTCLRNQYRCSNGNCINSIWCD FDNDCGDMSDER NCPTTVCDADTQ FRCQESGTCI 950
mSort	-----
Vps10p	-----
mCS2	-----
hCS3	-----
mCS3	-----
mCS1a	-----
mCS1b	-----
mCS1c	-----
hCS1	-----

..... : . . . . .

mSorLA	PL SYKCDLEDDCGD NSDESHCEMHQC RSDEFNCSSGMC IRSSWVCDGDND CRDWSDEANC 1010
mSort	-----SVG D AISVMVPDVYIS D-----DGGYS WAKMLEGPHY 522
Vps10p	-----TNDK EIVVTENKFDFK IQFYQYFDTVTDESLLMINSRGEA YISHDGGQTI 771
mCS2	-----NLGSQLVEYKEEMYITS-----DCGHT WRQVFEEHH 563
hCS3	-----NIGP ELSYTDIGVFISS-----DGGNT WRQIFDEEYN 611
mCS3	-----NIGS ELSYTDIGVFISS-----DGGNT WRQIFDEEYN 607
mCS1a	-----NIGS ELSDSDISMVSS-----DAGNT WRQIFEEHHS 587
mCS1b	-----NIGS ELSDSDISMVSS-----DAGNT WRQIFEEHHS 587
mCS1c	-----NIGS ELSDSDISMVSS-----DAGNT WRQIFEEHHS 587
hCS1	-----NIGS ELSDTDISMVSS-----DAGNT WRQIFEEHHS 587

: . . . . : . . . . .

mSorLA	TAIYHTCEASNFOCHNGHCIPQRWAC DGDADCQDGSDEDPVSCEKKCNF HCPNGTCIPS 1070
mSort	YT ILDSGGIIIVAE HSNRPINVIKFSTDEGQC-----WQSYVFTQE 563
Vps10p	RR FDSNGETIIEVFNPPYNNSSAYLF GSKGSIFS-----THDRGYSFMTA 816
mCS2	VL YLDHGGVIAAIK DTSIPLKILKFS VDEGHT-----WSTHNFTST 604

FIG 2D

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hCS3	VWFLDWGGALVAMKHTPLPVRH LWVSFDEGHS-----WDKYGFTSV 652
mCS3	VWFLDWGGALVAMK HTPLPVRHLWVS FDEGHS-----WDKYGFTLL 648
mCS1a	IL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
mCS1b	IL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
mCS1c	IL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
hCS1	VL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
. . . . .	
mSorLA	SK HCDGLRDCPDGS DEQHCEPFCTRFMDVFCNRRQQCLFHSMVCDGIVQC RDGSDEDAAF 1130
mSort	PI YFTGLASEPGA----- 576
Vps10p	KLPEARQLGMPLDF N----- 831
mCS2	SVFVDGLLSEPGD----- 617
hCS3	PLFVDGALVEAGM----- 665
mCS3	PLFVDGALVEAGV----- 661
mCS1a	PLFVDGVLGEPGE----- 641
mCS1b	PLFVDGVLGEPGE----- 641
mCS1c	PLFVDGVLGEPGE----- 641
hCS1	PLFVDGVLGEPGE----- 641
. . . . .	
mSorLA	AGCSQDPEFHKECDEFGQCQNGVCI SLIWKCDGMDDCGDYSDEANCENP TEAPNCSRYF 1190
mSort	-----RSMNISIW GFTESFITRQWV SYTVDFKDIL 606
Vps10p	-----AKAQDTFIYYGGRNCESILSPECHAVAYLTNDGGE TFTEMLDNAI 876
mCS2	-----ETLVMTVF GHIS--FRSDWE LVKVDFRPSF 645
hCS3	-----ETHIMTVF GHFS--LRSEWQ LVKVVDYKSIF 693
mCS3	-----ETHIMTVF GHFS--LRSEWQ LVKVVDYKSIF 689
mCS1a	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
mCS1b	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
mCS1c	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
hCS1	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
: : : : : . . . . .	
mSorLA	QF HCENGHCIPNRW KCDRENDGCDWS DEKDCGDSHVLP SPTPGPSTCLPNYFRCSGACV 1250
mSort	ER NCE-----EDDYTTWLAHSTD-----PGDYKDGC 633
Vps10p	HC EFAGSLFKYPSN EDMVMCQVKEKSSQTRSLVSSTDFQDDKNTVFENIIGYLSTGGYI 936
mCS2	PR QCG-----EDDYSSWD LTDL-----QGDDHCI 668
hCS3	SR HCT-----KEDYQTHW LLN-----QGEPCV 715
mCS3	SRRCT-----KEDFETWH LLN-----QGEPCV 711
mCS1a	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
mCS1b	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
mCS1c	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
hCS1	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
. . . . .	
mSorLA	MGTWVCDGYRDCAD GSDEEACPSLANSTAAPTQLGQCDFEFECHQPKKCI PNWKRC 1310
mSort	LG-----YKEQFLRLR 644
Vps10p	IVAVPHE-----NNELRAYVTID 954
mCS2	MG-----QORSYRKRK 679
hCS3	MG-----ERKIFKKRK 726
mCS3	MG-----ERKIFKKRK 722
mCS1a	MG-----AKRIYKKRK 702
mCS1b	MG-----AKRIYKKRK 702
mCS1c	MG-----AKRIYKKRK 702
hCS1	MG-----AKRIYKKRK 702

FIG 2E

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mSorLA      GHQDCQDQDE ANCPHSTLTCTSTREFKCEDGEAC IVLSERCDGFLD CSDESDEKACSDE 1370
mSort      KSSVCQNGRDYVVA KQPSVCPCSLED FLCDFGYFRPEN AS-----ECVE QPELKGHELE 698
Vps10p     GT EFAEAKFPYDED VGKQEAFTILES EKGSIFLHLATN LVPGRDFGNLLK SNSNGTSFVT 1014
mCS2       STSWCVKGRSFTSALTSRVCKCRSD FLCDYGFERSSSSESTA--NKCSA NFWFNPLSPP 737
hCS3       PG AQCALGRDHSGS VVSEPCVCANWD FECDYGYERHGE SQ-----CVPAFWYNPASPS 779
mCS3       PG AQCALGREYSGS VVSEPCVCADWD FECDYGYERHGE SQ-----CVPAFWYNPASPS 775
mCS1a      SE RKCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSLS 753
mCS1b      SE RKCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSLS 753
mCS1c      SE RKCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSLS 753
hCS1       SE RKCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSLS 754

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mSorLA      LT VYKVQNLQWTAD FSGDVTLTWMPR KKMPASACVYNV YYRVVGESIWK LETHSNTKTST 1430
mSort      FC LYGKEEHLTTNGYR-----KIPGDKCQGM N-----PAREVK----- 732
Vps10p     LE HAVNRNTFGYVD FEKIQGLEGI IL TNIVSNSDKVAEN KEDKQLKTKIT FNEGSDWN-- 1072
mCS2       ED CVLGQTYTSSLGYSR-----KVVSNVCEGGV DLQQSPVQLQCPLQAPR----- 781
hCS3       KD CSLGQSYLNSTGYR-----RIVSNNCTDGL REKYTAKAQMCPC GKAPR----- 823
mCS3       KD CSLGQSYLNSTGYR-----RIVSNNCTDGL RDKYSAKTQLCP GKAPR----- 819
mCS1a      KD CSLGQSYLNSAGYR-----KVVSNNCTDGV REQYTAKPQKCP GKAPR----- 797
mCS1b      KD CSLGQSYLNSAGYR-----KVVSNNCTDGV REQYTAKPQKCP GKAPR----- 797
mCS1c      KD CSLGQSYLNSAGYR-----KVVSNNCTDGV REQYTAKPQKCP GKAPR----- 797
hCS1       KD CSLGQSYLNSTGYR-----KVVSNNCTDGV REQYTAKPQKCP GKAPR----- 798

```

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mSorLA      VL KVLKPDTTYQVK VQVHCLNKVHNTNDFVTLRTPEGLPDAPRNLQLSLN REEEGVILGH 1490
mSort      -----DLKKKCTSNFL NPTKQN----- 749
Vps10p     -----FLKPPKRDS EGKFFCSCSKSL DECSLHLHGYTE RKDIRDTYSS 1115
mCS2       -----GLQVSIRGEAVAVRPREDVLFVV RQEQGDVLT 814
hCS3       -----GLHVVTTDGRLVAEQGHNATFIILMEEGDLQRT 856
mCS3       -----GLHVVTTDGRLVAEQGHNATFIILMEEGDLQRT 852
mCS1a      -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 830
mCS1b      -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 830
mCS1c      -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 830
hCS1       -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 831

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```

mSorLA      WAPPVHTHGLIREY IVEYSRSGSKMWASQRAASNSTEI KNLLLNALYTVR VAAVTSRGIG 1550
mSort      -----SKSNSVPIILAIVGLMLVTVVAG----- 772
Vps10p     GS ALGMMFGVGNVG PNLLPYKECSTFTTDDGETWAEV KKTPhQWEYGDHGGILVLPEN 1175
mCS2       KYQVDLGDGFKAMY VNLTLTGEPRIHHEYSPIYRVSV RAENMAGHDEAVLFVQVNSPLQ 874
hCS3       NI QLDFGDGIAVSY ANFSPIEDGIKH VYKSAGIFQVTA YAENNLGSDTAVFLHVVCPE 916
mCS3       NI QLDFGDGIAVSY ANFSPIEDGIKH VYKSAGIFQVTA YAENNLGSDTAVFLHVVCPE 912
mCS1a      LI QVDFGDGIAVSY VNLSSMEDGIKH VYQNVGIFRVTV QVDNSLGSASAVLYLHVTCPLE 890
mCS1b      LI QVDFGDGIAVSY VNLSSMEDGIKH VYQNVGIFRVTV QVDNSLGSASAVLYLHVTCPLE 890
mCS1c      LI QVDFGDGIAVSY VNLSSMEDGIKH VYQNVGIFRVTV QVDNSLGSASAVLYLHVTCPLE 890
hCS1       LI QVDFGDGIAVSY VNLSSMEDGIKH VYQNVGIFRVTV QVDNSLGSASAVLYLHVTCPLE 891

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mSorLA      NW SDSKSITTIKGV IYQAPNIHIDSY DENSLSFTLTMD GDIKVNGYVNLFWSDAHKQE 1610
mSort      -----VLIVKKYVCGGR- 784
Vps10p     SE TDSISYSTDFGK TWKDYKFCADKVLVKDITTVPRDS ALRFLLFGEAAD IGGSSFRITYT 1235
mCS2       AL YLEVVPVIGVNQ EVNLTAVLLPLN PNLTVFYWWIGHSLQPLSLDNSV TTKFTDAGDV 934

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FIG 2F

# Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

Inventor(s): Attie/Stoeck/Schueler/Clee

Application No.:

Docket Number: 960296.99080

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hCS3	HVHLRVPFVAIRNKEVNISAVVWPSQLGTLTYFWWFGNSTKPLITL DSSISFTFLAEGTD 976
mCS3	HV HLRVPFVAIRNK DVNISAVVWPSQ LGTLTYFWWFGNSTKPLITLDSSI SFTFLAEGTN 972
mCS1a	HV HLSLPFVTTKNK EVNATAVLWPSQ VGTLYVWWYGNNTPLITLEGSI SFKFTSEGMN 950
mCS1b	HV HLSLPFVTTKNK EVNATAVLWPSQ VGTLYVWWYGNNTPLITLEGSI SFKFTSEGMN 950
mCS1c	HV HLSLPFVTTKNK EVNATAVLWPSQ VGTLYVWWYGNNTPLITLEGSI SFKFTSEGMN 950
hCS1	HV HLSLPFVTTKNK EVNATAVLWPSQ VGTLYVWWYGNNTPLITLEGSI SFRFTSEGMN 951
. . . . .	
mSorLA	KK TLSFRGGSALSH KVSNLTAHTSYE ISAWAKTDLGDS PLAFEHILTRGSSPPAPSLKAK 1670
mSort	----FLVHRYSVLQQHAEADGVEALD STSHAKSGYHDD ----- 818
Vps10p	ID FRNIFERQCDFD ITGKESADYKYS PLSSKSNCLFGHQT----- 1275
mCS2	RV TVQAACGNSVLQ DSRLVRLDQFQ VVPLRFSRELDT ----- 972
hCS3	TI TVQVAAGNALIQ DTKEIAVHEYFQSLLSFSPNLDY ----- 1014
mCS3	TI TVQVAAGNALIQ DTKEIAVHEYFQSLLSFSPNLDY ----- 1010
mCS1a	TI TVQVSAGNAILQ DTKTIAVYEEFR SLRLAFSPNLDD ----- 988
mCS1b	TI TVQVSAGNAILQ DTKTIAVYEEFR SLRLAFSPNLDD ----- 988
mCS1c	TI TVQVSAGNAILQ DTKTIAVYEEFR SLRLAFSPNLDD ----- 988
hCS1	TI TVQVSAGNAILQ DTKTIAVYEEFR SLRLSFSPNLDD ----- 989
. . . . . : . . : . . . . .	
mSorLA	AI NQTAVECIWTGP KNVVYGIFYATS FLDLYRNPKSVTTSLHNKTIVIVSK DEQYLFLVRV 1730
mSort	-----SDEDLLE----- 825
Vps10p	-----EFLRKTDENC FIGNIPLSEF 1295
mCS2	-----FNPNTPEWR EDVGLVVTRL 991
hCS3	-----HNPDIPEWRKDIGNVIKRA 1033
mCS3	-----HNPDIPEWR QDIGNVIKRA 1029
mCS1a	-----YNPDIPEWRDISRVIKKS 1007
mCS1b	-----YNPDIPEWRDISRVIKKS 1007
mCS1c	-----YNPDIPEWRDISRVIKKS 1007
hCS1	-----YNPDIPEWRDIGRVIKKS 1008
: . . . . : . . . . : . . . . : . . . .	
mSorLA	LIPYQGPSSDYVVV KMIPDSRLPPRH LHAVHIGKTSALIKWESPYDSPDQ DLFYAIKVD 1790
mSort	-----
Vps10p	SR NIKNCSCTRQDF ECDYNFYKANDGTCKLVKGLSPAN AADVCKKEPDLI EYFESSGYRK 1355
mCS2	LS KETSIPEELLVT VVKPGLPTIADL YVLLPLPRPTRKRSLTS--DKRLAAVQQALNSHR 1049
hCS3	LV KVTSPEDQILIAVFPGLPTS AELFILPPKNLTERRKGNEGDLEQIVE TLFNALNQNL 1093
mCS3	LI KVTSPEDQILVAVFPGLPTS AELFILPPKNLTERRKGHEGDLEQIVE TLFNALNQNL 1089
mCS1a	LV EATGIPSQHILVAVLPGLPTAAELFVLPYQDGTREN KRSPEDLEQISE VLIHKLNQNL 1067
mCS1b	LV EATGIPSQHILVAVLPGLPTAAELFVLPYQDGTREN KRSPEDLEQISE VLIHKLNQNL 1067
mCS1c	LV EATGIPSQHILVAVLPGLPTAAELFVLPYQDGTREN KRSPEDLEQISE VLIHKLNQNL 1067
hCS1	LV EATGVPQHILVAVLPGLPTAAELFVLPYQDPAGEN KRSTDDLEQISE LLIHTLNQNS 1068
. . . . .	
mSorLA	LI RKTDRSYKVRSR NSTVEYSLSKLE PGGKYHIIIVQLGNMSKDSSIKITT VLSAPDALK 1850
mSort	-----
Vps10p	IPLSTCEGGLKLDAPSSPHACPGK-----EKE FKEYSVSAGPFAFIFISILLI 1404
mCS2	IS FILRGGLRILVE LRDTDTGP-----QRPGSGG-Y WAVVVLVFIG 1090
hCS3	VQ FELKPGVQVIVY VTQLTLAP-----LVDSSAGHSSSAMLMLLSVV 1135
mCS3	VQ FELKPGVQVIVY VTQLTLAP-----LVDSSAGHSSSAMLMLLSVV 1131
mCS1a	VH FELKPGVQVLVH AAHLTAAP-----LVDLTPTHSGSAMLMLLSVV 1109
mCS1b	VH FELKPGVQVLVH AAHLTAAP-----LVDLTPTHSGSAMLMLLSVV 1109
mCS1c	VH FELKPGVQVLVH AAHLTAAP-----LVDLTPTHSGSAMLMLLSVV 1109
hCS1	VH FELKPGVRVLVH AAHLTAAP-----LVDLTPTHSGSAMLMLLSVV 1110

FIG 2G



**FIG 2H**